

At page 8, line 1, please change "Table 2" to --Table 4--.

At page 11, lines 21-22, please change "Table 5 (A and B)" to --Table 5--.

At page 11, immediately before line 23, please insert the following text:

a2  
70180  
"SEQ ID NO: 544304560"  
--Table 5. Hybridization Probes for Regions of Human Slit-1.

Hybridization probe for first leucine rich repeat region	SEQ ID NO:01, nucleotides 82-828
Hybridization probe for second leucine rich repeat region	SEQ ID NO:01, nucleotides 829-1503
Hybridization probe for third leucine rich repeat region	SEQ ID NO:01, nucleotides 1504-2166
Hybridization probe for fourth leucine rich repeat region	SEQ ID NO:01, nucleotides 2167-2751
Hybridization probe for EGF repeats one to five	SEQ ID NO:01, nucleotides 2752-3327
Hybridization probe for the sixth EGF repeat and preceding spacer region	SEQ ID NO:01, nucleotides 3328-3461
Hybridization probe for the 99aa spacer/G-loop region	SEQ ID NO:01, nucleotides 3462-3987
Hybridization probe for EGF repeats seven to nine	SEQ ID NO:01, nucleotides 3988-4341
Hybridization probe for the cysteine knot region	SEQ ID NO:01, nucleotides 4342-4575

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Table 6. PCR Primers for regions of Human Slit.

PCR Primers for first leucine rich repeat region	Forward: SEQ ID NO:01, nucleotides 82-111 Reverse: reverse complement of SEQ ID NO:01, nucleotides 799-828
PCR Primers for second leucine rich repeat region	Forward: SEQ ID NO:01, nucleotides 829-858 Reverse: reverse complement of SEQ ID NO:01, nucleotides 1474-1503

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PCR Primers for third leucine  
rich repeat region

Forward: SEQ ID NO:01, nucleotides 1504-1533  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 2137-2166

PCR Primers for fourth leucine  
rich repeat region

Forward: SEQ ID NO:01, nucleotides 2167-2196  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 2722-2751

PCR Primers for EGF repeats  
one to five

Forward: SEQ ID NO:01, nucleotides 2752-2781  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 3298-3327

PCR Primers for the sixth EGF  
repeat and preceding spacer  
region

Forward: SEQ ID NO:01, nucleotides 3328-3357  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 3432-3461

PCR Primers for the 99aa  
spacer/G-loop region

Forward: SEQ I:01, nucleotides 3462-3491  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 3958-3987

PCR Primers for EGF repeats  
seven to nine

Forward: SEQ ID NO:01, nucleotides 3988-4017  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 4312-4341

PCR Primers for the cysteine  
knot region

Forward: SEQ ID NO:01, nucleotides 4342-4371  
Reverse: reverse complement of SEQ ID NO:01,  
nucleotides 4546-4575

Leucine rich repeats (LRRs) are predicted by comparison with known proteins and by the presence of a leucine rich core sequence. In slit proteins, the LRRs are flanked by conserved sequences referred to as the amino- and carboxy- flanking regions. These flanking regions are found in other known proteins, but only in a few instances are both the amino- and carboxy-flank regions present in a single protein. The so called "99aa spacer" is actually ~200 amino acids in the Drosophila protein and 174 amino acids in Human Slit-1. This region shows homology to the G-loops of laminin A chains.

Cysteine knots are dimerisation domains defined by the presence of six cysteine residues between which disulphide bridges form. The only absolutely conserved residues are the six cysteines, and spacing between them is highly variable, apart from between cysteines 2 and 3, and 5 and 6. The glycine between cysteines 2 and 3 is only present in a subset of cysteine knots.

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Drosophila slit and Human slit-1 both have an extra cysteine after cysteines 5 and 6: this may serve as an intermolecular bond. Human Slit-1 gene displays the overall structure of the Drosophila gene, and amino acid conservation is found along the entire length of the protein (48% homology at the amino acid sequence excluding the signal sequence; see below). The Human gene has an extra LRR between LRR2 and LRR3 of the first set of LRRs; in the third set, the Human gene has an extra LRR between LRR3 and LRR4. The Human gene has two extra EGF repeats, on either side of the seventh EGF repeat in Drosophila slit.

#### Isolation of Human slit-1

Searching of the EST database revealed an EST, ab16g10.r1, with homology to the 99aa spacer region of Drosophila slit. This EST was used to probe a Human fetal brain library (Stratagene), and clones for Human slit-1 were isolated.

#### Features of Human Slit Predicted Protein

0076694504500  
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Signal sequence	SEQ ID NO:02, residues 7-24
First amino-flanking sequence	SEQ ID NO:02, residues 28-59
First set of Leucine Rich Repeats	SEQ ID NO:02, residues 60-179 (6 repeats)
First carboxy-flanking sequence	SEQ ID NO:02, residues 180-276
Second amino-flanking sequence	SEQ ID NO:02, residues 277-308
Second set of Leucine Rich Repeats	SEQ ID NO:02, residues 309-434 (5 repeats)
Second carboxy-flanking sequence	SEQ ID NO:02, residues 435-501
Third amino-flanking sequence	SEQ ID NO:02, residues 502-533
Third set of Leucine Rich Repeats	SEQ ID NO:02, residues 534-560 (5 repeats)
Third carboxy-flanking sequence	SEQ ID NO:02, residues 661-722
Fourth amino-flanking sequence	SEQ ID NO:02, residues 723-754
Fourth set of Leucine Rich Repeats	SEQ ID NO:02, residues 755-855 (4 repeats)
Fourth carboxy-flanking sequence	SEQ ID NO:02, residues 856-917
First EGF repeat	SEQ ID NO:02, residues 918-952
Second EGF repeat	SEQ ID NO:02, residues 953-993
Third EGF repeat	SEQ ID NO:02, residues 994-1031

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Fourth EGF repeat	SEQ ID NO:02, residues 1032-1071
Fifth EGF repeat	SEQ ID NO:02, residues 1072-1109
Spacer	SEQ ID NO:02, residues 1110-1116
Sixth EGF repeat	SEQ ID NO:02, residues 1117-1153
"99aa spacer"	SEQ ID NO:02, residues 1155-1329
Seventh EGF repeat	SEQ ID NO:02, residues 1330-1366
Eighth EGF repeat	SEQ ID NO:02, residues 1367-1404
Nineth EGF repeat	SEQ ID NO:02, residues 1405-1447
Cysteine knot motif	SEQ ID NO:02, residues 1448-1525

#### Amino acid identity between Drosophila and Human Slit-1

First amino-flanking sequence	53%
First set of Leucine Rich Repeats	52% (54%, 67%, NA, 38%, 54%, 50%)
First carboxy-flanking sequence	42%
Second amino-flanking sequence	50%
Second set of Leucine Rich Repeats	60% (54%, 58%, 67%, 71%, 50%)
Second carboxy-flanking sequence	62%
Third amino-flanking sequence	56%
Third set of Leucine Rich Repeats	49% (46%, 46%, 42%, NA, 58%)
Third carboxy-flanking sequence	36%
Fourth amino-flanking sequence	53%
Fourth set of Leucine Rich Repeats	48% (25%, 58%, 46%, 63%)
Fourth carboxy-flanking sequence	63%
First EGF repeat	34%
Second EGF repeat	46%
Third EGF repeat	46%
Fourth EGF repeat	35%
Fifth EGF repeat	47%